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OICE

#8

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/776,874DATE: 02/22/2001
TIME: 10:35:09Input Set : A:\Seq.txt
Output Set: N:\CRF3\02222001\I776874.raw

ENTERED

SEQUENCE LISTING

2 (1) GENERAL INFORMATION:

3 (i) APPLICANT: Iris Pecker, Israel Vlodavsky and Elena
4 Feinstein5 (ii) TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE
6 HAVING HEPARANASE ACTIVITY AND EXPRESSION
7 OF SAME IN GENETICALLY MODIFIED CELLS

8 (iii) NUMBER OF SEQUENCES: 47

9 (iv) CORRESPONDENCE ADDRESS:

10 (A) ADDRESSEE: Mark M. Friedman c/o Anthony Castorina

11 (B) STREET: 2001 Jefferson Davis Highway, Suite 207

12 (C) CITY: Arlington

13 (D) STATE: Virginia

14 (E) COUNTRY: United States of America

15 (F) ZIP: 22202

16 (v) COMPUTER READABLE FORM:

17 (A) MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

18 (B) COMPUTER: Twinhead* Slimnote-890TX

19 (C) OPERATING SYSTEM: MS DOS version 6.2,
20 Windows version 3.1121 (D) SOFTWARE: Word for Windows version 2.0 converted to
22 an ASCII file

23 (vi) CURRENT APPLICATION DATA:

C--> 24 (A) APPLICATION NUMBER: US/09/776,874

C--> 25 (B) FILING DATE: 06-Feb-2001

26 (C) CLASSIFICATION:

27 (vii) PRIOR APPLICATION DATA:

28 (A) APPLICATION NUMBER: 08/922,170

29 (B) FILING DATE: 2 SEP 1997

30 (A) APPLICATION NUMBER: 09/109,386

31 (B) FILING DATE: 10 JUL 1998

32 (A) APPLICATION NUMBER: PCT/US98/17954

33 (B) FILING DATE: 31 AUG 1998

34 (viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: Friedman, Mark M.

36 (B) REGISTRATION NUMBER: 33,883

37 (C) REFERENCE/DOCKET NUMBER: 910/14

38 (ix) TELECOMMUNICATION INFORMATION:

39 (A) TELEPHONE: 972-3-5625553

40 (B) TELEFAX: 972-3-5625554

41 (C) TELEX:

43 (2) INFORMATION FOR SEQ ID NO: 1:

44 (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 27

46 (B) TYPE: nucleic acid

47 (C) STRANDEDNESS: single

48 (D) TOPOLOGY: linear

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Input Set : A:\Seq.txt
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```
C--> 49      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
50      CCATCCTAAT ACGACTCACT ATAGGGC 27
52 (2) INFORMATION FOR SEQ ID NO: 2:
53      (i) SEQUENCE CHARACTERISTICS:
54          (A) LENGTH: 24
55          (B) TYPE: nucleic acid
56          (C) STRANDEDNESS: single
57          (D) TOPOLOGY: linear
C--> 58      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
59      GTACTGATGC CATGTAACG AATC 24
61 (2) INFORMATION FOR SEQ ID NO: 3:
62      (i) SEQUENCE CHARACTERISTICS:
63          (A) LENGTH: 23
64          (B) TYPE: nucleic acid
65          (C) STRANDEDNESS: single
66          (D) TOPOLOGY: linear
C--> 67      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
68      ACTCACTATA GGGCTCGAGC GGC 23
70 (2) INFORMATION FOR SEQ ID NO: 4:
71      (i) SEQUENCE CHARACTERISTICS:
72          (A) LENGTH: 22
73          (B) TYPE: nucleic acid
74          (C) STRANDEDNESS: single
75          (D) TOPOLOGY: linear
C--> 76      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
77      GCATCTTAGC CGTCTTCTT CG 22
79 (2) INFORMATION FOR SEQ ID NO: 5:
80      (i) SEQUENCE CHARACTERISTICS:
81          (A) LENGTH: 15
82          (B) TYPE: nucleic acid
83          (C) STRANDEDNESS: single
84          (D) TOPOLOGY: linear
C--> 85      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
86      TTTTTTTTTT TTTT 15
88 (2) INFORMATION FOR SEQ ID NO: 6:
89      (i) SEQUENCE CHARACTERISTICS:
90          (A) LENGTH: 23
91          (B) TYPE: nucleic acid
92          (C) STRANDEDNESS: single
93          (D) TOPOLOGY: linear
C--> 94      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
95      TTCGATCCCA AGAAGGAATC AAC 23
97 (2) INFORMATION FOR SEQ ID NO: 7:
98      (i) SEQUENCE CHARACTERISTICS:
99          (A) LENGTH: 24
100         (B) TYPE: nucleic acid
101         (C) STRANDEDNESS: single
102         (D) TOPOLOGY: linear
C--> 103     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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```
104 GTAGTGATGC CATGTAAC TG AATC 24
106 (2) INFORMATION FOR SEQ ID NO: 8:
107 (i) SEQUENCE CHARACTERISTICS:
108 (A) LENGTH: 9
109 (B) TYPE: amino acid
110 (C) STRANDEDNESS: single
111 (D) TOPOLOGY: linear
C--> 112 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
113 Tyr Gly Pro Asp Val Gly Gln Pro Arg
114 5 9
116 (2) INFORMATION FOR SEQ ID NO: 9:
117 (i) SEQUENCE CHARACTERISTICS:
118 (A) LENGTH: 1721
119 (B) TYPE: nucleic acid
120 (C) STRANDEDNESS: double
121 (D) TOPOLOGY: linear
C--> 122 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
123 CTAGAGCTTT CGACTCTCCG CTGCGCGGCA GCTGGCGGGG GGAGCAGCCA GGTGAGCCCA 60
124 AGATGCTGCT GCGCTCGAAG CCTGCGCTGC CGCCGCCGCT SATGCTGCTG CTCCTGGGGC 120
125 CGCTGGGTCC CCTCTCCCTG GCGGCCCTGC CCCGACCTGC GCAAGCACAG GACGTCGTGG 180
C--> 126 ACCTGGACTT CTTCAACCGA GAGCCGCTGC ACCTGGTGAG CCCCTCGTTC CTGTCCGTC 240
127 CCATTGACGC CAACCTGGCC ACGGACCCGC GGTTCCTCAT CCTCTGGGT TCTCCAAAGC 300
128 TTCGTACCTT GGCAGAGGC TTGTCTCCTG CGTACCTGAG GTTGGTGCG ACCAAGACAG 360
129 ACTTCCTAAT TTTCGATCCC AAGAAGGAAT CAACCTTTGA AGAGAGAAGT TACTGGCAAT 420
130 CTCAAGTCAA CCAGGATATT TGCAAAATATG GATCCATCCC TCCTGATGTG GAGGAGAAGT 480
131 TACGGTTGGA ATGGCCCTAC CAGGAGCAAT TGCTACTCCG AGAACACTAC CAGAAAAAGT 540
132 TCAAGAACAG CACCTACTCA AGAAGCTCTG TAGATGTGCT ATACACTTTT GCAAACGCT 600
133 CAGGACTGGA CTTGATCTTT GGCCTAAATG CGTTATTAAG AACAGCAGAT TTGCACTGGA 660
134 ACAGTTCTAA TGCTCAGTTG CTCCTGGACT ACTGCTCTTC CAAGGGGTAT AACATTTCTT 720
135 GGGAACTAGG CAATGAACCT AACAGTTTCC TTAAGAAGGC TGAATTTTC ATCAATGGGT 780
136 CGCAGTTAGG AGAAGATTAT ATTCAATTGC ATAACTTCT AAGAAAGTCC ACCTTCAAAA 840
137 ATGCAAAACT CTATGGTCTT GATGTTGGTC AGCCTCGAAG AAAGACGGCT AAGATGCTGA 900
138 AGAGCTTCCT GAAGGCTGGT GGAGAAGTGA TTGATTCAGT TACATGGCAT CACTACTATT 960
139 TGAATGGACG GACTGCTACC AGGGAAGATT TTCTAAACCC TGATGATTTG GACATTTT 1020
140 TTTCATCTGT GCAAAAAGTT TTCCAGGTGG TTGAGAGCAC CAGGCCTGGC AAGAAGGTCT 1080
141 GGTTAGGAGA AACAAGCTCT GCATATGGAG GCGGAGCGCC CTTGCTATCC GACACCTTTG 1140
142 CAGCTGGGCT TATGTGGCTG GATAAATTGG GCCTGTCAGC CCGAATGGGA ATAGAAGTGG 1200
143 TGATGAGGCA AGTATTCTTT GGAGCAGGAA ACTACCATTT AGTGGATGAA AACTTCGATC 1260
144 CTTTACCTGA TTATTGGCTA TCTCTTCTGT TCAAGAAATT GGTGGGCACC AAGGTGTTAA 1320
145 TGGCAAGCGT GCAAGGTTCA AAGAGAAGGA AGCTTCGAGT ATACCTTCAT TGCACAAACA 1380
146 CTGACAATCC AAGGTATAAA GAAGGAGATT TAACTCTGTA TGCCATAAAC CTCCATAACG 1440
147 TCACCAAGTA CTTGCGGTTA CCCTATCCTT TTCTTAACAA GCAAGTGGAT AAATACCTTC 1500
148 TAAGACCTTT GGGACCTCAT GGATTACTTT CCAAACTGTG CCAACTCAAT GGTCTAACTC 1560
149 TAAAGATGGT GGATGATCAA ACCTTGCCAC CTTTAATGGA AAAACCTCTC CGGCCAGGAA 1620
150 GTTCACTGGG CTGCCCAGCT TTCTCATATA GTTTTTTGT GATAAGAAAT GCCAAAGTTG 1680
151 CTGCTTGCAT CTGAAAATAA AATATACTAG TCCTGACACT G 1721
153 (2) INFORMATION FOR SEQ ID NO: 10:
154 (i) SEQUENCE CHARACTERISTICS:
155 (A) LENGTH: 543
```

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```

156          (B) TYPE: amino acid
157          (C) STRANDEDNESS: single
158          (D) TOPOLOGY: linear
C--> 159      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
160 Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Leu Met Leu Leu
161          5          10          15
163 Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
164          20          25          30
166 Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
167          35          40          45
169 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
170          50          55          60
172 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
173          65          70          75          80
175 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
176          85          90          95
178 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
179          100         105         110
181 Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
182          115         120         125
184 Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
185          130         135         140
187 Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
188          145         150         155         160
190 Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe
191          165         170         175
193 Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
194          180         185         190
196 Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
197          195         200         205
199 Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
200          210         215         220
202 Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
203          225         230         235         240
205 Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser
206          245         250         255
208 Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
209          260         265         270
211 Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
212          275         280         285
214 Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
215          290         295         300
217 Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
218          305         310         315         320
220 Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
221          325         330         335
223 Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala
224          340         345         350
226 Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys

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```

227          355          360          365
229 Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val
230          370          375          380
232 Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
233 385          390          395          400
235 Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
236          405          410          415
238 Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
239          420          425          430
241 Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly
242          435          440          445
244 Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu
245          450          455          460
247 Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu
248 465          470          475          480
250 Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn
251          485          490          495
253 Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met
254          500          505          510
256 Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser
257          515          520          525
259 Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
260          530          535          540          543

```

262 (2) INFORMATION FOR SEQ ID NO: 11:

263 (i) SEQUENCE CHARACTERISTICS:

264 (A) LENGTH: 1721

265 (B) TYPE: nucleic acid

266 (C) STRANDEDNESS: double

267 (D) TOPOLOGY: linear

C--> 268 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```

270          CT AGA GCT TTC GAC 14
272 TCT CCG CTG CGC GGC AGC TGG CGG GGG GAG CAG CCA GGT GAG CCC AAG 62
274 ATG CTG CTG CGC TCG AAG CCT GCG CTG CCG CCG CCG CTG ATG CTG CTG 110
275 Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu
276          5          10          15
278 CTC CTG GGG CCG CTG GGT CCC CTC TCC CCT GGC GCC CTG CCC CGA CCT 158
279 Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
280          20          25          30
282 GCG CAA GCA CAG GAC GTC GTG GAC CTG GAC TTC TTC ACC CAG GAG CCG 206
283 Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
284          35          40          45
286 CTG CAC CTG GTG AGC CCC TCG TTC CTG TCC GTC ACC ATT GAC GCC AAC 254
287 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
288          50          55          60
290 CTG GCC ACG GAC CCG CGG TTC CTC ATC CTC CTG GGT TCT CCA AAG CTT 302
291 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
292 65          70          75          80
294 CGT ACC TTG GCC AGA GGC TTG TCT CCT GCG TAC CTG AGG TTT GGT GGC 350
295 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly

```

VERIFICATION SUMMARY
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Input Set : A:\Seq.txt
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L:24 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:25 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:49 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:58 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:67 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:76 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:85 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:94 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:103 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:112 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:122 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:126 M:111 C: (47) String data converted to upper case,
L:159 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:268 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:418 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:441 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:482 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:480 M:246 W: Invalid value of Alpha Sequence Header Field, [STRANDEDNESS:], SeqNo=14, value=[singl]
L:571 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:592 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=15
L:743 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:762 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:771 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:780 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:789 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:798 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:807 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:816 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:825 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:834 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:843 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:852 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:861 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:870 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:879 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:888 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:897 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:906 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:915 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:924 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:933 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:942 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:951 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:960 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:969 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:978 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:987 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]

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L:1893 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:1917 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=43
L:1949 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:2029 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:2093 M:111 C: (47) String data converted to upper case,
M:111 Repeated in SeqNo=45
L:2201 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:2217 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]